

FIG. 1

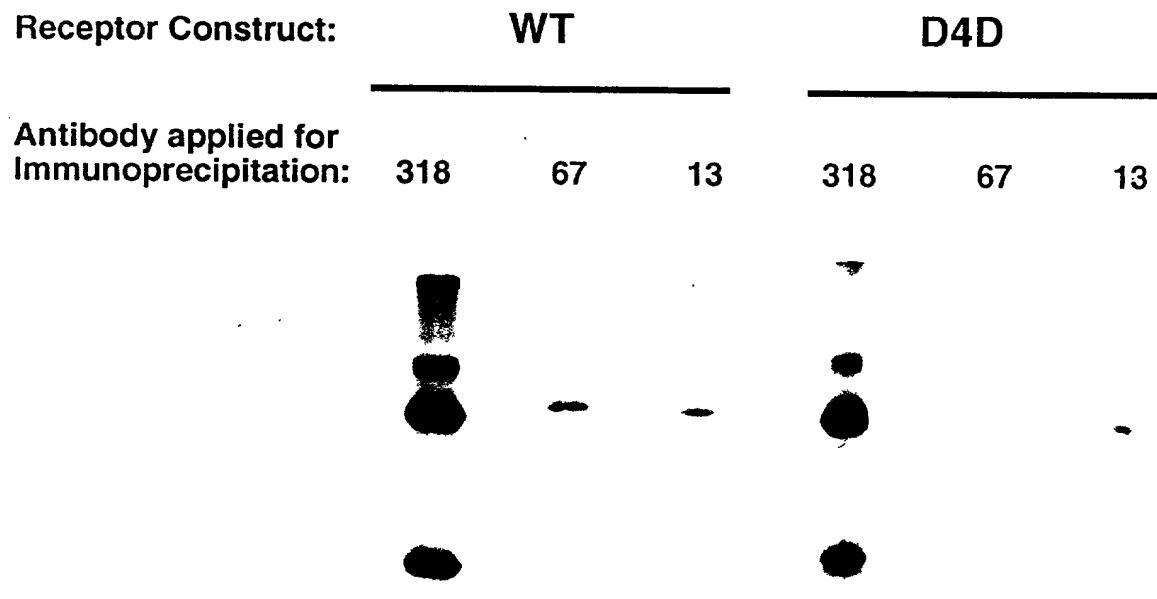


FIG. 2A

FIG. 2B

cag cca gtg tcc aca cga tcc caa cac acg cca act cca gaa ccc agc act gct cca agc acc
 Gln Pro Val Ser Thr Arg Ser Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr
 807 208

tcc ttc ctc cca atg ggc ccc agc ccc cca gct gaa ggg agc act ggc gac tcc gct ctt cca
 Ser Phe Leu Pro Met GLY Pro Ser Pro Pro Ala Glu Gly Ser Thr GLY Asp Phe Ala Leu Pro
 873 230

gtt gga ctg att gtg ggt gca gca ggc ttg ggt cta cta ata gga gtg gtg aac tgt gtc atc
 Val Gly Leu Ile Val Gly Val Thr Ala Leu Gly Leu Ile Gly Val Val Asn Cys Val Ile
 939 252

atg acc cag gtg aaa aag aag ccc ttg tgc ctg cag aga gaa GCC aag gtg cct cac ttg cct GCC
 Met Thr Gln Val Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro His Leu Pro Ala
 1005 274

gat aag gcc cgg ggt aca cag ggc ccc gag cag cag cac ctg ctg atc aca gca gcg ccg agc
 Asp Lys Ala Arg GLY Thr Gln Gly Pro Glu Gln Gln His Leu Leu II- Thr Ala Pro Ser Ser Ser
 1071 296

agc agc tcc ctg gag agc tcc gcc agt ggc ttg gag aga aag ggc ccc act cgg aac cag cca cag
 Ser Ser Leu Glu Ser Ser Ala Ser Ala Arg Arg Ala Pro Thr Arg Asn Gln Pro Gln
 1137 318

gca cca ggc gtg gag gcc agt ggg gcc gag ggc cgg ggc acc ggc tca gat tct tcc
 Gly Ala Gly Glu Ala Arg Ala Ser Thr Gly Ser Ser Asp Ser Ser Pro Gly Gly His Gly Thr Gln
 1203 340

ctt ggt ggc cat ggg acc cag gtc aat gtc acc tgc atc gtg aac gtc tgt agc agc tct gac cac
 Ala Pro Gly Val Glu Ala Ser Val Asn Val Thr Cys Ile Val Asn Val Cys Ser Ser Asp His
 1269 362

agc tca cag tgc tcc caa gcc agc tcc aca atg gga gac aca gat tcc agc ccc tcg gag tcc
 Ser Ser Gln Cys Ser Ser Gln Ala Ser Ser Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser
 1335 384

ccg aag gac gag cag gtc ccc ttc tcc aag gag gaa tgt gcc ttt cgg tca cag ctg gag acg cca
 Pro Lys Asp Glu Gln Val Pro Phe Ser Lys Glu Cys Ala Phe Arg Ser Gln Leu Glu Thr Pro
 1401 406

gag acc ctg ggg agc acc gaa gag aag ccc ctg ccc ctt gga gtg cct gat gct ggg atg aag
 Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro Leu Gly Val Pro Asp Ala Gly Met Lys
 1467 428

ccc agt taa ccaggccgtt gtgggtgtg tcgttagccaa ggtgggtgtg gcccggcag gatgaccctg cgaaggcc
 Pro Ser End 439

FIG. 3

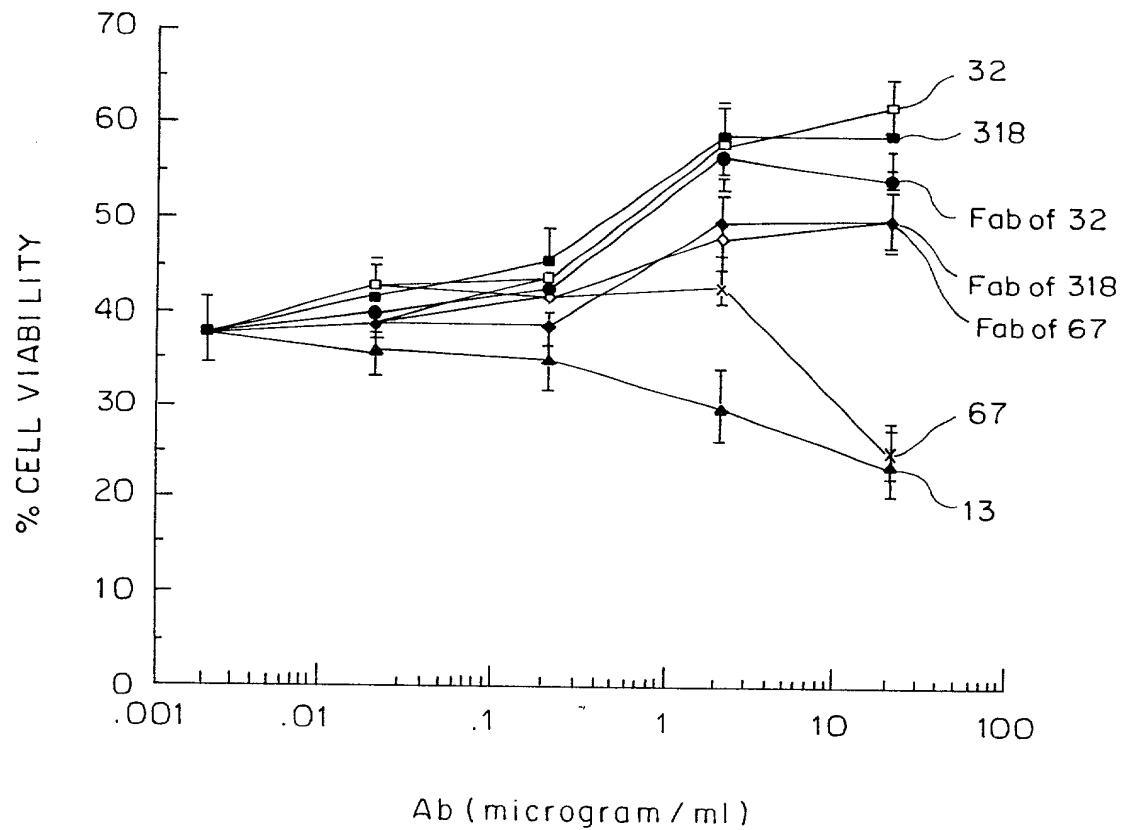


FIG. 4

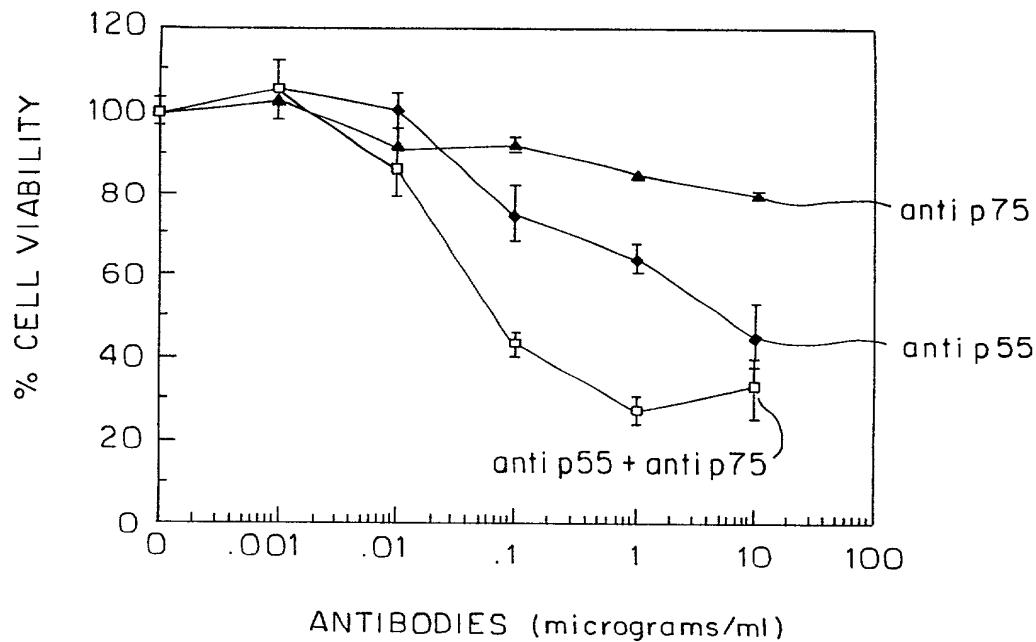


FIG. 5

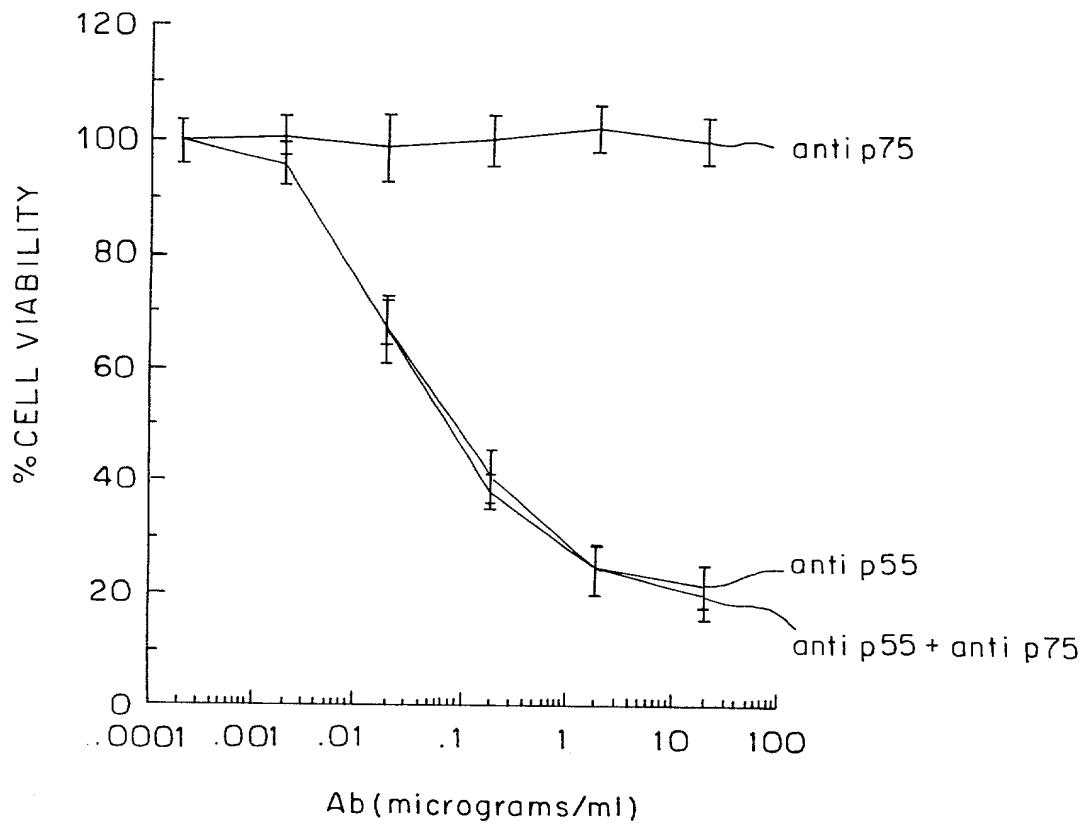


FIG. 6

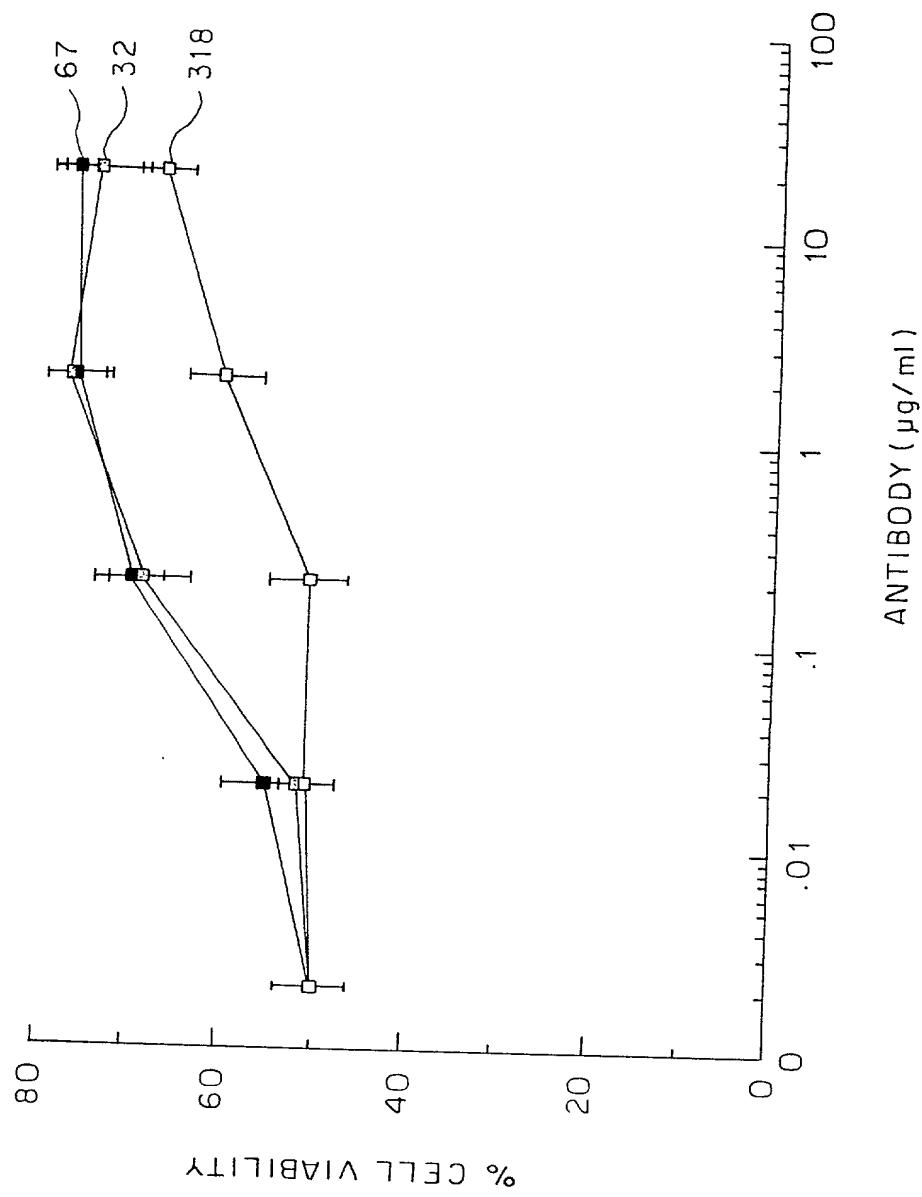


FIG. 7

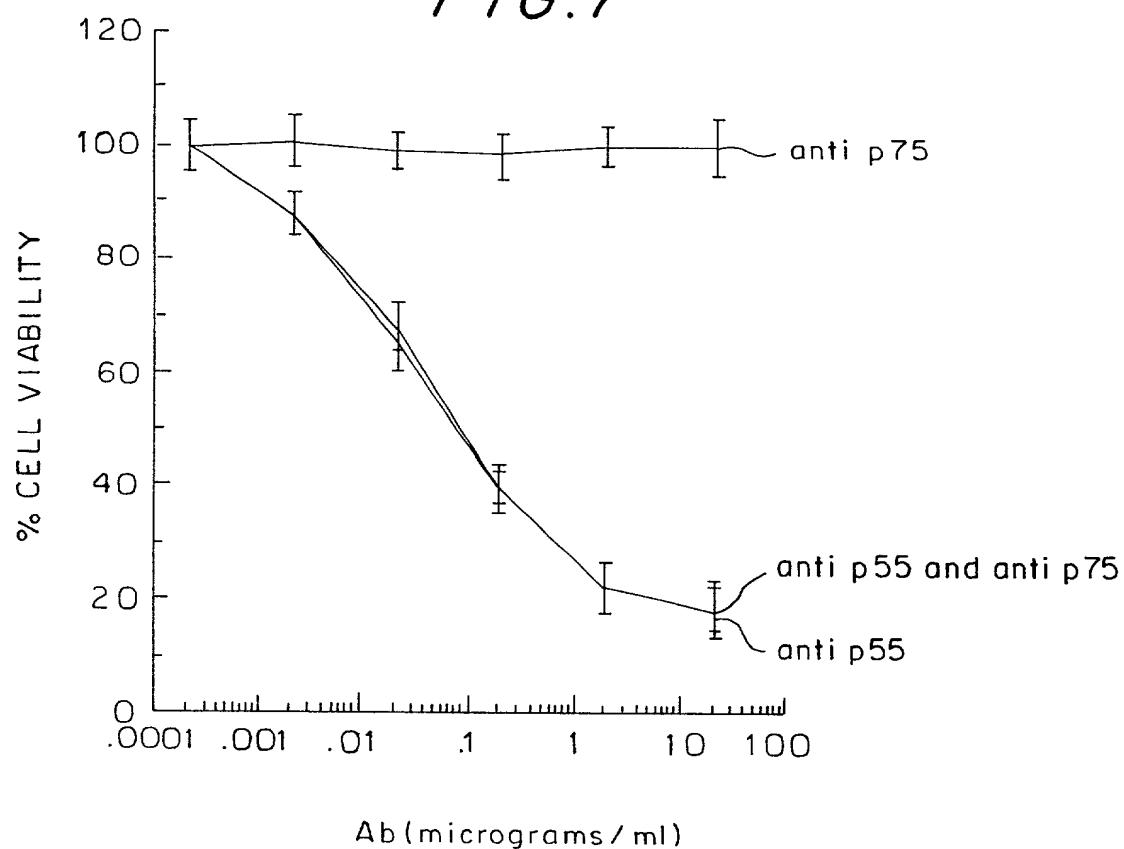


FIG. 8

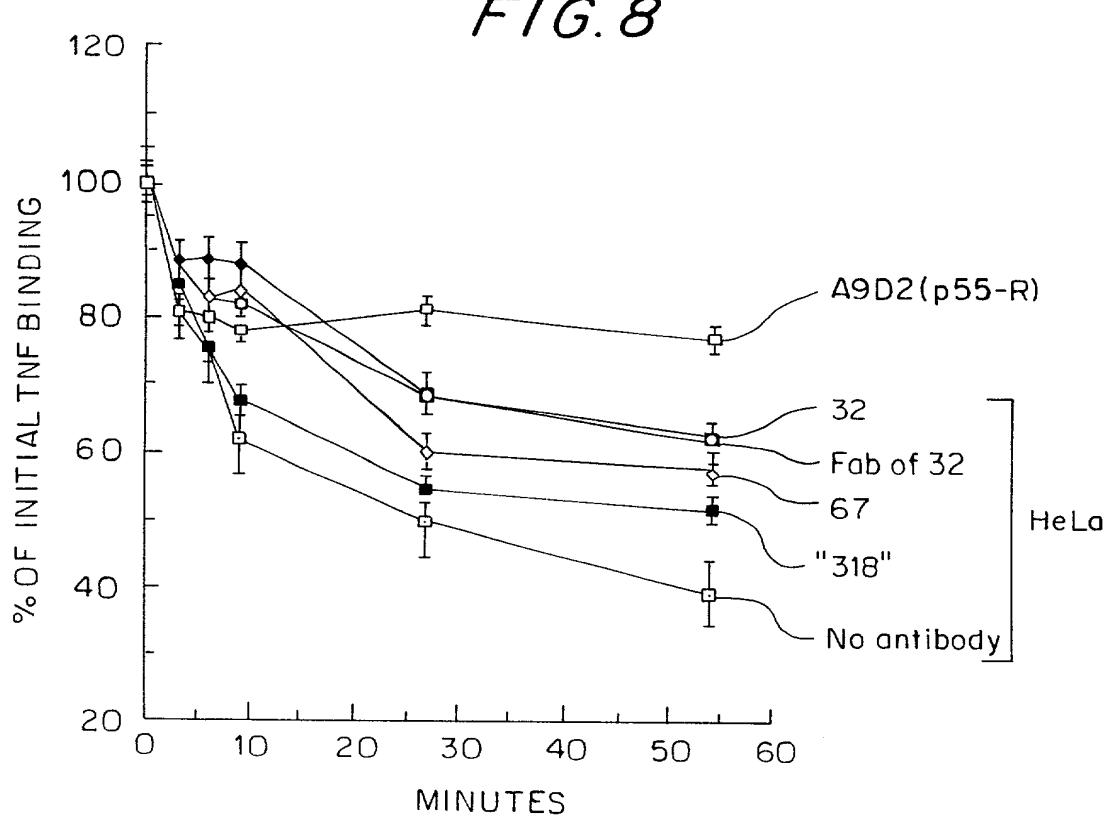


FIG. 9

hu p55 TNF-R (3-42)
 hu p75 TNF-R (39-76)
 hu FAS (31-67)
 hu NGF-R (3-37)
 hu CDw40 (25-60)
 rat Ox40 (25-60)

VCPQGKYIHPQNN---SIC
 TCRLREYYD-QTA---QMC
 QNLEGLH-ADGQF---CH-KPCPPGERKAR
 ACPTGLYTHSGE---CC-KACNLGEVAQP
 ACREKQYLIINSQ---CC-SLCQPGQKLVS
 NCVKDTPSGHK---CC-RECQPGHGMVSR
 --CDHT-RDTEVCH

hu p55 TNF-R (43-86)
 hu p75 TNF-R (77-119)
 hu FAS (68-112)
 hu NGF-R (38-80)
 hu CDw40 (61-104)
 rat Ox40 (61-104)

ECESGSEFTASEFHHL-RHCLSC-SKCRKENGG
 SCEDSTYQIWNWV-PECLSCGSRCISDD-QVETQACT
 PCQEKEYTDKAHFS SKRRC-RJCDDEGH
 PCLDSSVTSSDVVSATEPCPKPC-TECVGLOSHSAP
 PCGESEFLDITWRETN-CHQH-KYCDPNLGLRVQ
 PC-EPEGYNEAVNY-DTCKQG-TQCNRHS
 G-SELKQNCPT-EDTVCQ

hu p55 TNF-R (87-126)
 hu p75 TNF-R (120-162)
 hu FAS (113-149)
 hu NGF-R (81-119)
 hu CDw40 (105-144)
 rat Ox40 (105-123)

CRKNQYRHYWSENLFGCFC---SLCLHGT-VHLS
 CRPGWYCA-LSKQEGCRLCAPRKCRPGF
 CRPNEFCN-STVCEHCDPC-TKEHGI-IKE
 CAYGYQD-ETTGRCEAC-RVCEAGSG
 CEEGWHC-TSEACESCVLHRS
 CRFGTQP-RQDS-SHKLGYD

hu p55 TNF-R (127-155)
 hu p75 TNF-R (163-201)
 hu NGF-R (120-161)
 hu CDw40 (145-186)
 rat Ox40 (124-164)

TCHAGFFLR--ENE---CVS
 ECAPGTFESNTSST-DICRPH-QICN
 ECBDGTYSDDEAHV-DEPCLPQ-TVCE
 FCPVGFFSNVSSAF-EKCHP-TSCE
 ECPPGHESPGSSHQ-ACKPW-TNC
 TLSGKQIR-HPASNLSLDTYCE